
 W O R L D
 (TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Sat May 13 09:17:00 2000; MasPar time 3.04 Seconds
 Tabular output not generated. 124.592 Million cell updates/sec

Title: >US-09-331-631-27
 Description: (1-16) from US09331631.pep
 Perfect Score: 120
 Sequence: 1 OKHRSQILGCTYLXQOL 16

Scoring table: PAM 150
 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq35
 1:geneseqp

Statistics: Mean 19.307; Variance 54.468; scale 0.354

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	105	87.5	17	1	W62840	Stenocarpus sinuatus a	4.29e-05
2	64	53.3	195	1	R24944	Sequence of ovine trop	5.46e+00
3	64	53.3	195	1	R24941	Sequence of ovine trop	5.46e+00
4	64	53.3	195	1	P91396	Isoform of class II al	5.46e+00
5	64	53.3	195	1	R24945	Sequence of ovine trop	5.46e+00
6	60	50.0	195	1	R24943	Sequence of ovine trop	1.58e+01
7	59	49.2	23	1	W62839	Stenocarpus sinuatus a	2.05e+01
8	59	49.2	135	1	Y03782	S. aureus polypeptide	2.05e+01
9	59	49.2	377	1	R70029	Tobacco cluster-A prot	2.05e+01
10	57	47.5	195	1	R24942	Sequence of ovine trop	3.44e+01
11	57	47.5	195	1	R04540	Ovine tropoblast prot	3.44e+01
12	56	46.7	238	1	W81881	Enrllia sp. B82.3 pr	4.46e+01
13	55	45.8	111	1	W28096	Staphylococcus aureus	5.75e+01
14	55	45.8	222	1	Y05539	Wheat Type 1 glutathio	5.75e+01
15	55	45.8	396	1	W56695	Retracycline resistanc	5.75e+01
16	55	45.8	647	1	W34535	Helicoverpa armigera v	5.75e+01
17	55	45.8	647	1	R49662	Sequence of Heliothis	5.75e+01
18	54	45.0	201	1	W20604	H. pylori cytoplasmic	7.42e+01
19	54	45.0	410	1	R10693	Cephalosporin antibiotic	7.42e+01
20	54	45.0	706	1	W81353	Human hfrizled-6 prot	7.42e+01
21	53	44.2	47	1	W20493	H. pylori secreted or	9.54e+01
22	53	44.2	86	1	W20741	H. pylori secreted or	9.54e+01
23	53	44.2	119	1	R60515	Mouse beta-2 microglob	9.54e+01

ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
24	53	44.2	371	1	R70025	Tobacco chitinase enco	9.54e+01
25	53	44.2	1279	1	R60872	ST6-CFTR chimera H4.	9.54e+01
26	53	44.2	1279	1	R60873	ST6-CFTR chimera H5.	9.54e+01
27	52	43.3	161	1	W71485	Helicobacter polypepti	1.23e+02
28	52	43.3	195	1	R04539	cDNA clone of sequence	1.23e+02
29	52	43.3	544	1	W71203	Protein encoded by ORF	1.23e+02
30	52	43.3	802	1	R90848	Gibberellin (GA1), ent	1.23e+02
31	51	42.5	86	1	W26417	Swinepox virus HindIII	1.57e+02
32	51	42.5	331	1	W29817	Mammalian AMPK-gamma s	1.57e+02
33	51	42.5	349	1	W06416	Phosphotriesterase-rel	1.57e+02
34	51	42.5	725	1	W80363	The large subunit (RI)	1.57e+02
35	50	41.7	47	1	Y03000	Fragment of human secr	2.01e+02
36	50	41.7	72	1	Y02899	Fragment of human secr	2.01e+02
37	50	41.7	553	1	W10691	Newcastle disease viru	2.01e+02
38	50	41.7	553	1	W06828	Newcastle disease viru	2.01e+02
39	50	41.7	553	1	R49141	Newcastle disease viru	2.01e+02
40	50	41.7	572	1	W31273	Mouse frizzled-7 prote	2.01e+02
41	50	41.7	585	1	W31271	Human frizzled-5 prote	2.01e+02
42	50	41.7	666	1	W31268	Mouse frizzled-3 prote	2.01e+02
43	50	41.7	758	1	W97677	Human KDS2 protein kin	2.01e+02
44	50	41.7	1311	1	W72971	Precis coenia patched	2.01e+02
45	50	41.7	1311	1	W52197	Precis coenia (butterf	2.01e+02

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	W62840	standard; Protein; 17 AA.						
2	W62840	standard; Protein; 17 AA.						
3	W62840	standard; Protein; 17 AA.						
4	W62840	standard; Protein; 17 AA.						
5	W62840	standard; Protein; 17 AA.						
6	W62840	standard; Protein; 17 AA.						
7	W62840	standard; Protein; 17 AA.						
8	W62840	standard; Protein; 17 AA.						
9	W62840	standard; Protein; 17 AA.						
10	W62840	standard; Protein; 17 AA.						
11	W62840	standard; Protein; 17 AA.						
12	W62840	standard; Protein; 17 AA.						
13	W62840	standard; Protein; 17 AA.						
14	W62840	standard; Protein; 17 AA.						
15	W62840	standard; Protein; 17 AA.						
16	W62840	standard; Protein; 17 AA.						
17	W62840	standard; Protein; 17 AA.						
18	W62840	standard; Protein; 17 AA.						
19	W62840	standard; Protein; 17 AA.						
20	W62840	standard; Protein; 17 AA.						
21	W62840	standard; Protein; 17 AA.						
22	W62840	standard; Protein; 17 AA.						
23	W62840	standard; Protein; 17 AA.						
24	W62840	standard; Protein; 17 AA.						
25	W62840	standard; Protein; 17 AA.						
26	W62840	standard; Protein; 17 AA.						
27	W62840	standard; Protein; 17 AA.						
28	W62840	standard; Protein; 17 AA.						
29	W62840	standard; Protein; 17 AA.						
30	W62840	standard; Protein; 17 AA.						
31	W62840	standard; Protein; 17 AA.						
32	W62840	standard; Protein; 17 AA.						
33	W62840	standard; Protein; 17 AA.						
34	W62840	standard; Protein; 17 AA.						
35	W62840	standard; Protein; 17 AA.						
36	W62840	standard; Protein; 17 AA.						
37	W62840	standard; Protein; 17 AA.						
38	W62840	standard; Protein; 17 AA.						
39	W62840	standard; Protein; 17 AA.						
40	W62840	standard; Protein; 17 AA.						
41	W62840	standard; Protein; 17 AA.						
42	W62840	standard; Protein; 17 AA.						
43	W62840	standard; Protein; 17 AA.						
44	W62840	standard; Protein; 17 AA.						
45	W62840	standard; Protein; 17 AA.						

PF 29-NOV-1991; F00953.
 PR 29-NOV-1990; FR-014945.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (TRGE) TRANSGENE SA.
 PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
 PI Martal J, Reinaud P;
 DR WPI: 92-217070/26.
 PT New type I interferon variants with added N-terminal di:peptide -
 PT include expression cassettes providing high yield in yeast, esp.
 PT trophoblast derivs. with e.g. anti-luteolytic activity
 PS Claim 7; page 30; 53pp; French.
 CC The DNA sequence encoding the precursor of ovine trophoblastin was
 CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
 CC isoforms of trophoblastin. They have anti-luteolytic activity and
 CC are used to improve survival of transplanted embryos; as a reagent
 CC for detecting viability of embryos at an early stage of its
 CC development; and to improve the fertility of livestock.
 SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;
 Best Local Similarity 77.8%; Pred. No. 5.46e+00;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
 ||||| 1:1
 QY 8 LGCYLXQOL 16

RESULT 3

ID R24941 standard; Protein: 195 AA.

AC R24941;

DT 03-JAN-1992 (first entry)

DE Sequence of ovine trophoblastin.

KW Antiviral; antinflammatory; antitumour; immunomodulator; immunogen;

OS trophoblastin; antiluteolytic agent.

AM Ammotragus lervia.

FT Key Location/Qualifiers

FT peptide 1..23

FT /Label= signal

PN WO9209691-A.

PD 11-JUN-1992.

PF 29-NOV-1991; F00953.

PR 29-NOV-1990; FR-014945.

PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA (TRGE) TRANSGENE SA.

PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,

PI Martal J, Reinaud P;

DR WPI: 92-217070/26.

PT New type I interferon variants with added N-terminal di:peptide -

PT include expression cassettes providing high yield in yeast, esp.

PS trophoblast derivs. with e.g. anti-luteolytic activity

PS Disclosure; Fig 1; 53pp; French.

CC The DNA sequence encoding the precursor of ovine trophoblastin was

CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are

CC isoforms of trophoblastin. They have anti-luteolytic activity and

CC are used to improve survival of transplanted embryos; as a reagent

CC for detecting viability of embryos at an early stage of its

CC development; and to improve the fertility of livestock.

SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;

Best Local Similarity 77.8%; Pred. No. 5.46e+00;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
 ||||| 1:1
 QY 8 LGCYLXQOL 16

RESULT 4

ID P91396 standard; protein: 195 AA.

AC P91396;
 DT 15-FEB-1990 (first entry)
 DE Isoform of class II alpha-interferon trophoblastine precursor.
 KW Antiviral; antitumour.
 PN WO8908706-A.
 PD 21-SEP-1989.
 PF 17-MAR-1989; F00116.
 PR 18-MAR-1988; FR-003591.
 PA (INRG) Inst Nat Rech Agron.
 PI Martal J, Charpigny G, Gaye P, Pernollet J, Charlier M, Guillemot M,
 PI Huot J, Reinaud P, Hue D, Chene N, La Bonnardiere C;
 DR WPI: 89-292521/40.
 PT New isoform(s) of the class II alpha interferon trophoblastine
 PT - with eg antiviral, antitumour and immuno-modulating activities, and
 PT new DNA encoding sequences.
 PS Claim 11; page 11; 47pp; French.
 CC The isoform (23 kD) can be used for immunological, rejection-inhibiting,
 CC and cell differentiation activities. It can inhibit luteolysis at the
 CC start of pregnancy, monitor embryo viability, and protect embryos during
 CC transfer to the womb of a recipient.
 SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;
 Best Local Similarity 77.8%; Pred. No. 5.46e+00;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
 ||||| 1:1
 QY 8 LGCYLXQOL 16

RESULT 5

ID R24945 standard; Protein: 195 AA.

AC R24945;

DT 03-JAN-1992 (first entry)

DE Sequence of ovine trophoblastin variant Xd.

KW Antiviral; antinflammatory; antitumour; immunomodulator; immunogen;

OS trophoblastin; antiluteolytic agent.

AM Ammotragus lervia.

FT Key Location/Qualifiers

FT peptide 1..23

FT /Label= signal

PN WO9209691-A.

PD 11-JUN-1992.

PF 29-NOV-1991; F00953.

PR 29-NOV-1990; FR-014945.

PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA (TRGE) TRANSGENE SA.

PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,

PI Martal J, Reinaud P;

DR WPI: 92-217070/26.

PT New type I interferon variants with added N-terminal di:peptide -

PT include expression cassettes providing high yield in yeast, esp.

PS trophoblast derivs. with e.g. anti-luteolytic activity

PS Claim 7; page 30; 53pp; French.

CC The DNA sequence encoding the precursor of ovine trophoblastin was

CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are

CC isoforms of trophoblastin. They have anti-luteolytic activity and

CC are used to improve survival of transplanted embryos; as a reagent

CC for detecting viability of embryos at an early stage of its

CC development; and to improve the fertility of livestock.

SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;

Best Local Similarity 77.8%; Pred. No. 5.46e+00;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
 ||||| 1:1
 QY 8 LGCYLXQOL 16

```

RESULT 6
ID R24943 standard; Protein: 195 AA.
AC R24943:
DE 03-JAN-1992 (first entry)
DE Sequence of ovine trophoblastin variant Xb
KW Antiviral; antinflammatory; antitumor; immunomodulator; immunogen;
KW trophoblastin; antileukolytic agent.
OS Ammotragus lervia.
FH Key Location/Qualifiers
FT peptide 1..23
FT /label= signal
PN WO9209691-A.
PD 11-JUN-1992.
PF 29-NOV-1991; F00953.
PR 29-NOV-1990; FR-014945.
PR 29-NOV-1990; FR-014946.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (TRGE) TRANSENE SA.
PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
PI Marial J, Reinaud P;
PI WPI: 92-217070/26.
PT New type I interferon variants with added N-terminal dipeptide -
PT include expression cassettes providing high yield in yeast, esp.
PT trophoblast derivs with e.g. anti-leukolytic activity
PS Claim 7; page 30; 53pp; French.
CC The DNA sequence encoding the precursor of ovine trophoblastin was
CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
CC isoforms of trophoblastin. They have anti-leukolytic activity and
CC are used to improve survival of transplanted embryos; as a reagent
CC for detecting viability of embryos at an early stage of its
CC development; and to improve the fertility of livestock.
SQ Sequence 195 AA;

Query Match
Best Local Similarity 50.0%; Score 60; DB 1; Length 195;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 22 LGCYLSERL 30
OY 8 LGCYLXQOL 16

RESULT 7
ID W62839 standard; Protein: 23 AA.
AC W62839:
DE 27-OCT-1998 (first entry)
DE Stenocarpus sinuatus antimicrobial protein.
KW Antimicrobial protein; Infestation; control.
OS Stenocarpus sinuatus.
PN WO9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NJ, Goulter KC, Green JL, Mannens JM, Marcus JP;
PI WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 65; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
OS Sequence 23 AA;

Query Match
Best Local Similarity 49.2%; Score 59; DB 1; Length 23;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

DB 10 RGEILCEYRLCOO 22
OY 4 RSOILGCT-LXQO 15

```

```

RESULT 8
ID Y03782 standard; Protein: 135 AA.
AC Y03782:
DE 11-JUN-1999 (first entry)
DE S. aureus polypeptide.
KW Staphylococcus aureus polypeptide; thyroiditis; infective carditis;
KW lung abscess; secretory diarrhoea; cerebral abscess; conjunctivitis;
KW toxic shock syndrome; folliculitis; septic arthritis; antibacterial;
KW H pylori infection; gastric ulcer; adenocarcinoma.
OS Staphylococcus aureus.
PN EP-905243-A2.
PD 31-MAR-1999.
PF 03-AUG-1998; 306185.
PR 05-AUG-1997; US-055387.
PA (SMK) SMITHKLINE BEECHAM CORP.
PA (SMK) SMITHKLINE BEECHAM PLC.
PI Burnham MKR, Lonetto MA, Warren PV;
PI WPI: 99-19267/17.
DR N-PSDB: X31852.
PT New essential polypeptides from Staphylococcus aureus useful for
PT treating diseases such as infective endocarditis and toxic shock
PT syndrome
PS Claim 11; Page 24-25; 70pp; English.
CC The invention provides new Staphylococcus aureus polypeptides (Y03781-94)
CC and the genes (X31851-864) encoding them. Host cells containing vectors
CC comprising the nucleic acid sequences are used for the recombinant
CC expression of the proteins. The polypeptides can be used to screen for
CC modulators for use in antibacterial therapy. The polypeptides, their
CC antagonists and agonists are used to prevent or treat diseases caused by
CC S. aureus such as thyroiditis, lung abscesses, infective carditis,
CC secretory diarrhoea, cerebral abscesses, conjunctivitis, toxic shock
CC syndrome, folliculitis and septic arthritis. Screening for the presence of
CC the polypeptides may be used to diagnose, predict the susceptibility to,
CC or stage the progress of these S. aureus diseases and diseases caused by
CC Helicobacter pylori such as gastric ulcers and gastric adenocarcinoma.
CC There is not much information known about the essential genes expressed
CC by S. aureus during infection but these new polypeptides have been
CC identified as essential. They can therefore be used to develop
CC antibacterial compounds specific for these essential genes and this
CC ensures the effectiveness of the compounds in killing S. aureus. In
CC addition, these polypeptides can be used to effectively diagnose and
CC treat infections and diseases caused by S. aureus without the risk of
CC development of antibiotic resistance. The present sequence represents a
CC S. aureus polypeptide which has homology to a B. subtilis probable
CC acetyltransferase.
SQ Sequence 135 AA;

Query Match
Best Local Similarity 49.2%; Score 59; DB 1; Length 135;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

DB 42 HMKRRTSGYLYXKOF 57
OY 1 QKHSQILGCTLXQOL 16

RESULT 9
ID R70029 standard; Protein: 377 AA.
AC R70029:
DE 29-SEP-1995 (first entry)
DE Tobacco cluster-A protein encoded by genomic clone.
KW Tobacco; chitinase; antifungal; fungicide; Cluster-A.
OS Nicotiana tabacum.
FH Key Location/Qualifiers
FT peptide 1..25
FT /label= signal
FT /label= signal peptide
FT misc_difference 28..29
FT /note= "CDNA encodes additional ile here"
FT misc_difference 188..201
FT /label= Determined by sequencing the protein
FT misc_difference 222..247
FT /note= "Determined by sequencing the protein"
PN EP-639642-A.

```

PD 22-FEB-1995.
 PF 17-AUG-1993; 202425.
 PR 17-AUG-1993; EP-202425.
 PA (MOGE-) MOGEN INT NV.
 PA (UTLE-) RIJKSUNIV LEIDEN.
 PI Apotheker-de Groot M, Bol JF, Cornelissen BJC, Linthorst HJM;
 PI Meijchers LS, Ponstein AS, Sela-buurlage MB;
 DR WPI: 95-083454/12.
 DR N-PSDB: 082976.
 PT New plant protein having endo-chitinase activity - used in
 PT antifungal compns. and to develop transformed plants which are
 PT less susceptible to fungal infection.
 PS Claim 25-28; 43pp; English.
 CC Screening of a lambda ZAP cDNA library of TMV-infected Samsun NN
 CC tobacco plants with a probe derived from PROB40 (a partial Cluster-A
 CC cDNA clone) resulted in the isolated of 11 positively hybridising
 CC clones. Analysis revealed that all were identical and corresp. to
 CC Cluster-A cDNA. The sequence of cDNA clone CA-3 is given in 082973/
 CC R10025. A genomic library of N. tabacum was screened using the
 CC Cluster-A cDNA insert of clone CA-3 as a probe (see 082977, 082978).
 CC The complete nt. sequence of Cluster-A cDNA including the deduced
 CC primary structure of the Cluster-A protein the 5' and 3' UTR regions
 CC of the gene are shown in 082976/R70029. Comparison of the cDNA
 CC clone with the Cluster-A gene revealed that these sequences share
 CC a high degree of identity (94%). The Cluster-A precursor protein
 CC contains a putative signal peptide as well as 4 potential N-linked
 CC glycosylation sites (N-X-S/T). The predicted mature protein has
 CC a calculated mol. wt. of 39,033 Da.
 SQ Sequence 377 AA;

Query Match 49.2%; Score 59; DB 1; Length 377;
 Best Local Similarity 60.0%; Pred. No. 2.05e+01;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 11 IFSCFLXQOL 20
 1:1111111
 QY 7 IUGCTLXQOL 16

RESULT 10
 ID R24942 standard; Protein; 195 AA.
 AC R24942;
 DT 03-JAN-1992 (first entry)
 DE Sequence of ovine trophoblastin variant Xa.
 KW Antiviral; antinflammatory; antitumour; immunomodulator; immunogen;
 KW trophoblastin; antitumolytic agent.
 OS Ammotragus lervia.
 FH Key Location/Qualifiers
 FT peptide 1..23
 FT /label= signal
 PN WO9209691-A.
 PD 11-JUN-1992.
 PE 29-NOV-1991; F00953.
 PR 29-NOV-1990; FR-014945.
 PR 29-NOV-1990; FR-014946.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (FRGE) TRANGENE SA.
 PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
 PI Martal J, Reinard P,
 DR WPI: 92-217070/26.
 PT New type I interferon variants with added N-terminal dipeptide -
 PT include expression cassettes providing high yield in yeast, esp.
 PT trophoblast derivs. with e.g. anti-luteolytic activity
 PS Claim 7; page 30; 53pp; French.
 CC The DNA sequence encoding the precursor of ovine trophoblastin was
 CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
 CC isoforms of trophoblastin. They have anti-luteolytic activity and
 CC are used to improve survival of transplanted embryos; as a reagent
 CC for detecting viability of embryos at an early stage of its
 CC development; and to improve the fertility of livestock.
 SQ Sequence 195 AA;

Query Match 47.5%; Score 57; DB 1; Length 195;

Best Local Similarity 66.7%; Pred. No. 3.44e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 22 LGCYLSRKL 30
 11111111
 QY 8 LGCYLXQOL 16

RESULT 11
 ID R04540 standard; Protein; 195 AA.
 AC R04540;
 DT 17-SEP-1990 (first entry)
 DE Ovine trophoblast protein-1 (OTF-1).
 KW Bovine trophoblast protein-1; btp-1; fertility; ds.
 OS Sus scrofa
 PN EP-367063-A.
 PD 9-MAY-1990.
 PE 23-OCT-1989; 119642.
 PR 26-OCT-1988; US-262870.
 PA (UMOR) Univ of Missouri.
 PI Roberts MR, Imakawa K;
 DR WPI: 90-141062/19.
 DR N-PSDB: 004289
 PT Recombinant bovine trophoblast protein-1 -
 PT used for enhancing fertility or treating viral diseases in
 PT mammals, esp. cattle.
 PS Disclosure: P; English.
 CC The btp-1 produced from the gene may be used to promote fertility
 CC or treat viral disease in cattle. The gene may also be used to
 CC provide transgenic animals with enhanced fertility, or in
 CC prophylactic and therapeutic treatment of other mammals.
 SQ Sequence 195 AA;

Query Match 47.5%; Score 57; DB 1; Length 195;
 Best Local Similarity 66.7%; Pred. No. 3.44e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 22 LGCYLSRKL 30
 11111111
 QY 8 LGCYLXQOL 16

RESULT 12
 ID W81981 standard; Protein; 238 AA.
 AC W81981;
 DT 02-MAR-1999 (first entry)
 DE Ehrlichia sp. E82.3 protein.
 KW Granulocytic ehrlichia; GE; E82; tick-borne infection; fatal; vaccine;
 KW Immune response; detection; diagnosis; Ehrlichiosis.
 OS Ehrlichia sp.
 PN WO9849312-A2.
 PD 05-NOV-1998.
 PR 24-APR-1998; U08264.
 PR 25-APR-1997; US-044869.
 PA (AQU1-) AQUITA BIOPHARMACEUTICALS INC.
 PI Beltz G, Coughlin RT, Murphy C, Storey J;
 DR WPI: 99-034653/03.
 DR N-PSDB: V65142.
 PT New isolated granulocytic ehrlichia nucleic acids - used to develop
 PT products for use in vaccines for inhibiting Ehrlichiosis and for use
 PT in detection and diagnosis
 PS Claim 1a; Fig 10; 184pp; English.
 CC This sequence encodes the E82.3 protein which is associated with and has
 CC been isolated from HE80 cells infected with Ehrlichia sp. GE is an acute
 CC potentially fatal tick borne infection and the proteins described in
 CC this invention can be used in vaccines to elicit a beneficial immune
 CC response in an animal to GE. They can be used for inhibiting Ehrlichiosis
 CC in an animal. The products can also be used for detection and diagnosis.
 SQ Sequence 238 AA;

Query Match 46.7%; Score 56; DB 1; Length 238;
 Best Local Similarity 54.5%; Pred. No. 4.46e+01;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 204 QILGFLRHL 214
 1111 : : :
 QY 6 QILGCLXKQL 16

RESULT 13
 ID W28096 standard; Protein: 111 AA.
 AC W28096;
 DE 01-SEP-1998 (first entry)
 DE Staphylococcus aureus protein of unknown function.
 KM Staphylococcus aureus protein: ribozyme; antisense sequence; control;
 KM Staphylococcal gene; regulatory element; bacterial gene expression;
 KM vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
 KM toxic shock syndrome.
 OS Staphylococcus aureus.
 FT Key Location/Qualifiers
 FT Misc_difference 1. 111
 FT /note="residues designated X are not defined in
 FT the specification"

MO9730070-A1.
 PN 21-AUG-1997.
 PD 19-FEB-1997: U02318.
 PR 20-FEB-1996: US-011888.
 PA (SMK) SMTKLIN BECHAM CORP.
 PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
 PI Pratt JM, Relchard RW, Rosenberg M, Ward JM;
 DR WPI: 97-424969/39.
 DR N-PSDB: T84032.
 PT Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used
 PT to isolate antimicrobial compounds, and in vaccines against S.
 PT aureus infection
 PS Claim 6: Page 463: 989pp: English.
 CC The present sequence represents a Staphylococcus aureus protein of
 CC unknown function. The DNA sequence was isolated from a library of
 CC clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can
 CC be used in the construction of ribozymes and antisense sequences to
 CC control the expression of Staphylococcal genes. The DNA sequence is
 CC also useful as a source of regulatory elements for the control of
 CC bacterial gene expression. The present protein may be used to produce
 CC vaccines to enable a host to produce specific antibodies with
 CC antibacterial action. These vaccines and antibodies would protect
 CC a host against invasion by S. aureus, and conditions relating to
 CC Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled
 CC skin syndrome, and toxic shock syndrome.
 SQ Sequence 111 AA;

Query Match 45.8%; Score 55; DB 1; Length 111;
 Best Local Similarity 85.7%; Pred No. 5.75e+01;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 7 CYLKQL 13
 111111
 QY 10 CYLKQL 16

RESULT 14
 ID Y05539 standard; Protein: 222 AA.
 AC Y05539;
 DE 05-JUL-1999 (first entry)
 DE Wheat Type I glutathione transferase subunit IC2.
 KM Glutathione transferase; GST; glutathione peroxidase; wheat; WIC2;
 KM IC2; herbicide resistance; transgenic plant.
 OS Triticum aestivum.
 PN MO9914337-A2.
 PD 25-MAR-1999.
 PR 16-SEP-1998: G02802.
 PR 16-SEP-1997: GB-019727.
 PA (RHON) RHON-POULENC AGRIC LTD.
 PI Cole DJ, Cummins I, Edwards R;
 DR WPI: 99-244035/20.
 DR N-PSDB: X25146.
 PT New isolated glutathione transferase subunit polynucleotides

PS Claim 3; Page 83: 101pp: English.
 CC The present sequence represents IC2, a wheat glutathione transferase
 CC (GST) subunit that resembles the type I GSTs from maize. Clone
 CC WIC2 (see X25146), which codes for IC2, was isolated from a cDNA
 CC expression library prepared from fenclorazole-ethyl (herbicide
 CC salene) treated wheat shoots using maize GST antiserum.
 CC Recombinant IC2 shows activity toward herbicides and non-herbicide
 CC substrates, and also has glutathione peroxidase activity toward
 CC organic hydroperoxides. The invention provides cDNAs and genomic
 CC DNAs (see X25144-52) encoding wheat GST subunits (see Y05537-45)
 CC active in herbicide metabolism. This is fundamental to
 CC understanding GST detoxification in wheat and in the development
 CC of transgenic herbicide resistant plants expressing wheat GSTs.
 CC The invention also provides methods of identifying compounds
 CC capable of metabolism by GST, or compounds that induce GST
 CC expression in gramineaceous plants, and for determining the GST
 CC level in a sample of seed or flour. Transgenic plants, host cells
 CC used for production of GST subunits and GST dimeric proteins, and
 CC vectors are also provided.
 SQ Sequence 222 AA;

Query Match 45.8%; Score 55; DB 1; Length 222;
 Best Local Similarity 50.0%; Pred No. 5.75e+01;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 78 RKHPELLGC 87
 :1111111111
 QY 1 QKRSQILGC 10

RESULT 15
 ID W56695 standard; Protein: 396 AA.
 AC W56695;
 DE 24-JUL-1998 (first entry)
 DE Tetracycline resistance sequence contained in plasmid PRZTL1.
 KM Tn5 transposase; modified; enzyme; in vitro transposition; mutant;
 KM target; marker; transposon 5; plasmid PRZTL1; tetracycline resistance.
 OS Synthetic.
 OS Escherichia coli.
 PN MO9810077-A1.
 PD 12-MAR-1998.
 PR 09-SEP-1997: U15941.
 PR 02-MAY-1997: US-850880.
 PR 09-SEP-1996: US-814877.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 PI Goryshin IV, Reznikoff WS, Zhou H;
 DR WPI: 98-193627/17.
 DR N-PSDB: V28398.
 PT Modified Tn5 transposase construct used in novel system for in vitro
 PT transposition - used to, e.g. create absolute defective mutants,
 PT provide selective markers and to facilitate insertion of specialised
 PT DNA sequences into target DNA
 PS Disclosure: Pages 35-46: 73pp: English.
 CC This tetracycline resistance sequence is contained in the plasmid
 CC PRZTL1 which is used to demonstrate in vitro transposition of a
 CC transposable element located between a pair of Tn5 (transposon 5)
 CC outside end (OE) termini. The invention provides a genetic construct
 CC that contains a nucleotide sequence encoding a modified Tn5 transposase
 CC enzyme that has both greater avidity for Tn5 OE repeats and is less
 CC likely to assume an inactive multimeric form than a wild type Tn5
 CC transposase and a transposable DNA sequence flanked at its 5' and 3' ends
 CC by an 18 or 19 base pair flanking DNA sequence comprising nucleotide A
 CC at position 10, T at 11 and A at 12. The modified Tn5 transposase and
 CC the transposable DNA which is a DNA donor molecule are used in a system
 CC for in vitro transposition. The system and method can be used to create
 CC absolute defective mutants, to provide selective markers to target DNA,
 CC to provide portable regions of homology to a target DNA, to facilitate
 CC insertion of specialised DNA sequences into target DNA, to provide primer
 CC binding sites or tags for DNA sequencing, to facilitate production of
 CC genetic fusion for gene expression studies and protein domain mapping, as
 CC well as to bring together other desired combinations of DNA sequences
 CC (combinatorial genetics). The modified Tn5 transposase facilitates in
 CC vitro transposition reaction rates of at least about 100-fold higher

CC than can be achieved using wild type transposase (as measure in vivo).
 CC In vitro transposition using this system can also use donor DNA and
 CC target DNA that is circular or linear. The system also requires no
 CC outside high energy source and no other protein other than the modified
 CC transposase.
 SO Sequence 396 AA;

Query Match 45.8%; Score 55; DB 1; Length 396;
 Best Local Similarity 55.6%; Pred. No. 5.75e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 175 LIGCFLMOE 183
 Oy 7 ILGCVLX00 15

Search completed: Sat May 13 09:17:07 2000
 Job time : 7 secs.